

Figure 1. Sequence of full length C1 (ILKAP) and C1 clone.

09935124-082101

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1  ggcaaccaggcccgctgctgcccgcgggggtgtggagcccgccgctgctcgccggctgagtgctgtgctgctgctgcccctccaccagcctccgc 100
101 c  ATG GAC CTC TTC GGG GAC CTG CCG GAG CCC GAG CGC TCG CCG CGC CCG GCT GCC GGG AAA GAA GCT CAG AAA 173
1  M  D  L  F  G  D  L  P  E  P  E  R  S  P  R  P  A  A  G  K  E  A  Q  K  24
174 GGA CCC CTG CTC TTT GAT GAC CTC CCT CCG GCC AGC AGT ACT GAC TCA GGA TCA GGG GGA CCT TTG CTT TTT GAT 248
25 G  P  L  L  F  D  D  L  P  P  A  S  S  T  D  S  G  S  G  G  P  L  L  F  D  49
249 GAT CTC CCA CCC GCT AGC AGT GGC GAT TCA GGT TCT CTT GCC ACA TCA ATA TCC CAG ATG GTA AAG ACT GAA GGG 323
50 D  L  P  P  A  S  S  G  D  S  G  S  L  A  T  S  I  S  Q  M  V  K  T  E  G  74
324 AAA GGA GCA AAG AGA AAA ACC TCC GAG GAA GAG AAG AAT GGC AGT GAA GAG CTT GTG GAA AAG AAA GTT TGT AAA 398
75 K  G  A  K  R  K  T  S  E  E  E  K  N  G  S  E  E  L  V  E  K  K  V  C  K  99
399 GCC TCT TCG GTG ATC TTT GGT CTG AAG GGC TAT GTG GCT GAG CGG AAG GGT GAG AGG GAG GAG ATG CAG GAT GCC 473
100 A  S  S  V  I  F  G  L  K  G  Y  V  A  E  R  K  G  E  R  E  E  M  Q  D  A  124
474 CAC GTC ATC CTG AAC GAC ATC ACC GAG GAG TGT AGG CCC CCA TCG TCC CTC ATT ACT CGG GTT TCA TAT TTT GCT 548
125 H  V  I  L  N  D  I  T  E  E  C  R  P  P  S  S  L  I  T  R  V  S  Y  F  A  149
549 GTT TTT GAT GGA CAT GGA GGA ATT CGA GCC TCA AAA TTT GCT GCA CAG AAT TTG CAT CAA AAC TTA ATC AGA AAA 623
150 V  F  D  G  H  G  I  R  A  S  K  F  A  A  Q  N  L  H  Q  N  L  I  R  K  174
624 TTT CCT AAA GGA GAT GTA ATC AGT GTA GAG AAA ACC GTG AAG AGA TGC CTT TTG GAC ACT TTC AAG CAT ACT GAT 698
175 F  P  K  G  D  Y  I  S  V  E  K  T  V  K  R  C  L  L  D  T  F  K  H  T  D  199
699 GAA GAG TTC CTT AAA CAA GCT TCC AGC CAG AAG CCT GCC TGG AAA GAT GGG TCC ACT GCC ACG TGT GTT CTG GCT 773
200 E  E  F  L  K  Q  A  S  S  Q  K  P  A  W  K  D  G  S  T  A  T  C  V  L  A  224
774 GTA GAC AAC ATT CTT TAT ATT GCC AAC CTC GGA GAT AGT CGG GCA ATC TTG TGT CGT TAT AAT GAG GAG AGT CAA 848
225 V  D  N  I  L  Y  I  A  N  L  G  D  S  R  A  I  L  C  R  Y  N  E  E  S  Q  249
849 AAA CAT GCA GCC TTA AGC CTC AGC AAA GAG CAT AAT CCA ACT CAG TAT GAA GAG CGG ATG AGG ATA CAG AAG GCT 923
250 K  H  A  A  L  S  L  S  K  E  H  N  P  T  Q  Y  E  E  R  M  R  I  Q  K  A  274
924 GGA GGA AAC GTC AGG GAT GGG CGT GTT TTG GGC GTG CTA GAG GTG TCA CGC TCC ATT GGG GAC GGG CAG TAC AAG 998

275 G  G  N  V  R  D  G  R  V  L  G  V  L  E  V  S  R  S  I  G  D  G  Q  Y  K  299
999 CGC TGC GGT GTC ACC TCT GTG CCC GAC ATC AGA CGC TGC CAG CTG ACC CCC AAT GAC AGG TTC ATT TTG TTG GCC 1073
300 R  C  G  V  T  S  V  P  D  I  R  R  C  Q  L  T  P  N  D  R  F  I  L  L  A  324
1074 TGT GAT GGG CTC TTC AAG GTC TTT ACC CCA GAA GAA GCC GTG AAC TTC ATC TTG TCC TGT CTC GAG GAT GAA AAG 1148
325 C  D  G  L  F  K  V  F  T  P  E  E  A  V  N  F  I  L  S  C  L  E  D  E  K  349
1149 ATC CAG ACC CGG GAA GGG AAG TCC GCA GCC GAC GCC CGC TAC GAA GCA GCC TGC AAC AGG CTG GCC AAC AAG GCG 1223
350 I  Q  T  R  E  G  K  S  A  A  D  A  R  Y  E  A  A  C  N  R  L  A  N  K  A  374
1224 GTG CAG CGG GGC TCG GCC GAC AAC GTC ACT GTG ATG GTG GTG CGG ATA GGG CAC TGA_ggggtggcgcggccaggagcac 1304
375 V  Q  R  G  S  A  D  N  V  T  V  M  V  V  R  I  G  H  393
1305 gcattggtattgacttaaaaggttcattttgtgtgtgtgcacattgtgtgtttttgtgtactcctgtgggactccccatggttgaataaagggtttctcttt 1404
1405 tttttcctaaaaaaaaa 1422

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